AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.
What is claimed is:

1-12 Cancelled

13. (Currently amended) A method of detecting a severe acute respiratory syndrome coronavirus in a sample, the method comprising:

(a) contacting nucleic acids from the sample in at least one nucleic acid amplification reaction with at least one primer nucleic acid ~~comprising at least one nucleic acid~~ selected from the group consisting of: SEQ ID NOS: 11 and 22 and full complements thereof, further comprising at least one additional primer nucleic acid selected from the group consisting of: SEQ ID NOS: 12 and 20 ~~SEQ ID NOS: 1-12 and 15-24~~ and full complements thereof ~~in at least one nucleic acid amplification reaction~~; and,

(b) detecting the nucleic acids and/or one or more amplicons thereof from the nucleic acid amplification reaction during or after (a),

thereby detecting the severe acute respiratory syndrome coronavirus in the sample.

14. (Original) The method of claim 13, wherein at least one of the primer nucleic acids comprises a modified primer nucleic acid.

15. (Original) The method of claim 13, wherein at least one of the amplicons is about 440 nucleotides in length.

16. Cancelled

17. Cancelled

18. (Original) The method of claim 13, wherein the nucleic acid amplification reaction comprises a nested polymerase chain reaction.

19. (Original) The method of claim 13, wherein at least one of the primer nucleic acids comprises at least one label.

20. (Original) The method of claim 19, wherein (b) comprises detecting a detectable signal produced by the label, or amplifying a detectable signal produced by the label to produce an amplified signal and detecting the amplified signal.

21. (Currently amended) The method of claim 13, wherein (b) comprises monitoring binding between the amplicons and at least one oligonucleotide ~~having a sequence~~ selected from the group consisting of: SEQ ID NO: 27 and SEQ ID NO: 28 ~~SEQ ID NOS: 1-12 and 15-24~~, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NO: 27 and SEQ ID NO: 28 ~~SEQ ID NOS: 1-12 and 15-24~~, and full complements of SEQ ID NO: 27 and SEQ ID NO: 28 ~~SEQ ID NOS: 1-12 and 15-24~~ and the variant.

22. (Original) The method of claim 21, wherein the oligonucleotide comprises at least one label and/or at least one quencher moiety.

23. Cancelled

24. (Currently amended) A method of determining a presence of a severe acute respiratory syndrome coronavirus in a sample, the method comprising:

(a) contacting nucleic acids and/or amplicons thereof from the sample with one or more oligonucleotides ~~that comprise at least one nucleic acid with a sequence~~ selected from the group consisting of: ~~SEQ ID NOS: 1-12 and 15-24,~~ SEQ ID NOS: 11 and 22 and full complements thereof, and a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 11 and 22 and full complements thereof,

further comprising one or more oligonucleotides selected from the group consisting of: SEQ ID NOS: 12 and 20 and full complements thereof, and a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 12 and 20 and full complements thereof, ~~SEQ ID NOS: 1-12 and 15-24, and complements of SEQ ID NOS: 1-12 and 15-24 and the variant; and,~~
further comprising at least one oligonucleotide selected from the group consisting of: SEQ ID NO: 27 and SEQ ID NO: 28, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NO: 27 and SEQ ID NO: 28, and full complements of SEQ ID NO: 27 and SEQ ID NO: 28 and the variant, and

(b) monitoring binding between the nucleic acids and/or amplicons thereof, and the oligonucleotides, wherein detectable binding between the nucleic acids and/or amplicons thereof, and the oligonucleotides, determines the presence of the severe acute respiratory syndrome coronavirus in the sample.

25. (Original) The method of claim 24, wherein (a) comprises contacting the nucleic acids and/or amplicons thereof with the oligonucleotides in solution at a temperature of at least 42°C for at least 15 minutes, wherein a total weight of the solution comprises about 50% formalin and comprises heparin at a concentration of about 1 mg/ml.

26. (Original) The method of claim 24, comprising repeating (a) and (b) at least once using at least one additional sample and comparing the binding between the nucleic acids and/or amplicons thereof, and the oligonucleotides, of (b) with at least one repeated (b).

27. (Original) The method of claim 24, wherein at least one segment of the nucleic acids is amplified prior to or during (a) using at least one nucleic acid amplification technique to produce the amplicons and (b) comprises monitoring the binding between the nucleic acids and/or amplicons thereof, and the oligonucleotides, during or after amplification.

28. (Currently amended) A composition comprising a sample derived from a subject and at least one oligonucleotide ~~that comprises a nucleic acid with a sequence~~ selected from the group

consisting of: ~~SEQ ID NOS: 1-12 and 15-24~~ SEQ ID NOS: 11 and 22, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of ~~SEQ ID NOS: 1-12 and 15-24~~ SEQ ID NOS: 11 and 22, and full complements of ~~SEQ ID NOS: 1-12 and 15-24~~ SEQ ID NOS: 11 and 22 and the variant, ~~which oligonucleotide consists of 100 or fewer nucleotides.~~

further comprising at least one oligonucleotide selected from the group consisting of: SEQ ID NOS: 12 and 20, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 12 and 20, and full complements of SEQ ID NOS: 12 and 20 and the variant.

29. (Currently amended) A kit, comprising:

(a) at least one oligonucleotide ~~that comprises a nucleic acid with a sequence~~ selected from the group consisting of: SEQ ID NOS: 11 and 22, ~~SEQ ID NOS: 1-12 and 15-24,~~ a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 11 and 22, ~~SEQ ID NOS: 1-12 and 15-24,~~ and full complements of SEQ ID NOS: 11 and ~~22 SEQ ID NOS: 1-12 and 15-24~~ and the variant, ~~which oligonucleotide consists of 100 or fewer nucleotides;~~

further comprising at least one oligonucleotide selected from the group consisting of: SEQ ID NOS: 12 and 20, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 12 and 20, and full complements of SEQ ID NOS: 12 and 20 and the variant;

and one or more of:

(b) instructions for determining a presence of a severe acute respiratory syndrome coronavirus in a sample by monitoring binding between nucleic acids and/or amplicons thereof from the sample and the oligonucleotide, wherein the presence of the severe acute respiratory syndrome coronavirus in the sample is unknown or unsubstantiated; or,

(c) at least one container for packaging at least the oligonucleotide.

30. (Original) The kit of claim 29, further comprising at least one enzyme.

31. (Currently amended) A system for detecting a severe acute respiratory syndrome coronavirus in a sample, comprising:

(a) at least one oligonucleotide ~~that comprises a nucleic acid with a sequence~~ selected from the group consisting of: SEQ ID NOS: 11 and 22, ~~SEQ ID NOS: 1-12 and 15-24,~~ a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 11 and 22, ~~SEQ ID NOS: 1-12 and 15-24,~~ and full complements of SEQ ID NOS: 11 and 22 ~~SEQ ID NOS: 1-12 and 15-24~~ and the variant, ~~which oligonucleotide consists of 100 or fewer nucleotides;~~
further comprising at least one oligonucleotide selected from the group consisting of: SEQ ID NOS: 12 and 20, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 12 and 20, and full complements of SEQ ID NOS: 12 and 20 and the variant;

(b) at least one detector that detects binding between nucleic acids and/or amplicons thereof from the sample and the oligonucleotide; and,

(c) at least one controller operably connected to the detector, which controller comprises one or more instructions sets that correlate the binding detected by the detector with a presence of the severe acute respiratory syndrome coronavirus in the sample.

32. Cancelled